RAW SEQUENCE LISTING   DATE: 06/23/2003
PATENT APPLICATION: **US/09/908,992A** TIME: 14:58:13

Input Set : **A:\Hmv05401.app**
Output Set: **N:\CRF4\06232003\I908992A.raw**

```
 3 <110> APPLICANT: SYKEN, JOSH
 4         MUNGER, KARL
 6 <120> TITLE OF INVENTION: METHODS AND REAGENTS TO REGULATE APOPTOSIS
 8 <130> FILE REFERENCE: HMV-054.01
10 <140> CURRENT APPLICATION NUMBER: 09/908,992A
11 <141> CURRENT FILING DATE: 2001-07-19
13 <150> PRIOR APPLICATION NUMBER: 60/219,718
14 <151> PRIOR FILING DATE: 2000-07-19
16 <150> PRIOR APPLICATION NUMBER: 60/219,537
17 <151> PRIOR FILING DATE: 2000-07-20
19 <160> NUMBER OF SEQ ID NOS: 29
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 2656
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (32)..(1471)
32 <400> SEQUENCE: 1
33 gaattcgcgg ccgcagagtc cccgggccaa g atg gct gcg cgg tgc tcc aca      52
34                                   Met Ala Ala Arg Cys Ser Thr
35                                    1                   5
37 cgc tgg ttg ctg gtg gtt gtg ggg acc ccg cgg ctg ccg gct ata tcg    100
38 Arg Trp Leu Leu Val Val Val Gly Thr Pro Arg Leu Pro Ala Ile Ser
39         10                  15                  20
41 ggt aga ggg gcc cgg ccg ccc agg gag ggc gtg gtg ggg gca tgg ctg    148
42 Gly Arg Gly Ala Arg Pro Pro Arg Glu Gly Val Val Gly Ala Trp Leu
43         25                  30                  35
45 agc cgc aag ctg agc gtc ccc gcc ttt gcg tct tcc ctg acc tct tgc    196
46 Ser Arg Lys Leu Ser Val Pro Ala Phe Ala Ser Ser Leu Thr Ser Cys
47 40                  45                  50                  55
49 ggc ccc cga gcg ctg ctg aca ttg aga cct ggt gtc agc ctt aca gga    244
50 Gly Pro Arg Ala Leu Leu Thr Leu Arg Pro Gly Val Ser Leu Thr Gly
51                  60                  65                  70
53 aca aaa cat aac cct ttc att tgt act gcc tcc ttc cac acg agt gcc    292
54 Thr Lys His Asn Pro Phe Ile Cys Thr Ala Ser Phe His Thr Ser Ala
55              75                  80                  85
57 cct ttg gcc aaa gaa gat tat tat cag ata tta gga gtg cct cga aat    340
58 Pro Leu Ala Lys Glu Asp Tyr Tyr Gln Ile Leu Gly Val Pro Arg Asn
59          90                  95                  100
61 gcc agc cag aaa gag atc aag aaa gcc tat tat cag ctt gcc aag aag    388
62 Ala Ser Gln Lys Glu Ile Lys Lys Ala Tyr Tyr Gln Leu Ala Lys Lys
```

```
 63      105                    110                  115
 65 tat cac cct gac aca aat aag gat gat ccc aaa gcc aag gag aag ttc    436
 66 Tyr His Pro Asp Thr Asn Lys Asp Asp Pro Lys Ala Lys Glu Lys Phe
 67 120                    125                  130                135
 69 tcc cag ctg gca gaa gcc tat gag gtt ttg agt gat gag gtg aag agg    484
 70 Ser Gln Leu Ala Glu Ala Tyr Glu Val Leu Ser Asp Glu Val Lys Arg
 71                    140                  145                150
 73 aag cag tac gat gcc tac ggc tct gca ggc ttc gat cct ggg gcc agc    532
 74 Lys Gln Tyr Asp Ala Tyr Gly Ser Ala Gly Phe Asp Pro Gly Ala Ser
 75                    155                  160                165
 77 ggc tcc cag cat agc tac tgg aag gga ggc ccc act gtg gac ccc gag    580
 78 Gly Ser Gln His Ser Tyr Trp Lys Gly Gly Pro Thr Val Asp Pro Glu
 79             170                  175                180
 81 gag ctg ttc agg aag atc ttt ggc gag ttc tca tcc tct tca ttt gga    628
 82 Glu Leu Phe Arg Lys Ile Phe Gly Glu Phe Ser Ser Ser Ser Phe Gly
 83             185                  190                195
 85 gat ttc cag acc gtg ttt gat cag cct cag gaa tac ttc atg gag ttg    676
 86 Asp Phe Gln Thr Val Phe Asp Gln Pro Gln Glu Tyr Phe Met Glu Leu
 87 200                    205                  210                215
 89 aca ttc aat caa gct gca aag ggg gtc aac aag gag ttc acc gtg aac    724
 90 Thr Phe Asn Gln Ala Ala Lys Gly Val Asn Lys Glu Phe Thr Val Asn
 91                    220                  225                230
 93 atc atg gac acg tgt gag cgc tgc aac ggc aag ggg aac gag ccc ggc    772
 94 Ile Met Asp Thr Cys Glu Arg Cys Asn Gly Lys Gly Asn Glu Pro Gly
 95             235                  240                245
 97 acc aag gtg cag cat tgc cac tac tgt ggc ggc tcc ggc atg gaa acc    820
 98 Thr Lys Val Gln His Cys His Tyr Cys Gly Gly Ser Gly Met Glu Thr
 99             250                  255                260
101 atc aac aca ggc cct ttt gtg atg cgt tcc acg tgt agg aga tgt ggt    868
102 Ile Asn Thr Gly Pro Phe Val Met Arg Ser Thr Cys Arg Arg Cys Gly
103         265                  270                  275
105 ggc cgc ggc tcc atc atc ata tcg ccc tgt gtg gtc tgc agg gga gca    916
106 Gly Arg Gly Ser Ile Ile Ile Ser Pro Cys Val Val Cys Arg Gly Ala
107 280                    285                  290                295
109 gga caa gcc aag cag aaa aag cga gtg atg atc cct gtg cct gca gga    964
110 Gly Gln Ala Lys Gln Lys Lys Arg Val Met Ile Pro Val Pro Ala Gly
111                    300                  305                310
113 gtc gag gat ggc cag acc gtg agg atg cct gtg gga aaa agg gaa att   1012
114 Val Glu Asp Gly Gln Thr Val Arg Met Pro Val Gly Lys Arg Glu Ile
115             315                  320                325
117 ttc att acg ttc agg gtg cag aaa agc cct gtg ttc cgg agg gac ggc   1060
118 Phe Ile Thr Phe Arg Val Gln Lys Ser Pro Val Phe Arg Arg Asp Gly
119         330                  335                  340
121 gca gac atc cac tcc gac ctc ttt att tct ata gct cag gct ctt ctt   1108
122 Ala Asp Ile His Ser Asp Leu Phe Ile Ser Ile Ala Gln Ala Leu Leu
123         345                  350                  355
125 ggg gga aca gcc aga gcc cag ggc ctg tac gag acg atc aac gtg acg   1156
126 Gly Gly Thr Ala Arg Ala Gln Gly Leu Tyr Glu Thr Ile Asn Val Thr
127 360                    365                  370                375
```

RAW SEQUENCE LISTING   DATE: 06/23/2003
PATENT APPLICATION: US/09/908,992A   TIME: 14:58:14

Input Set : A:\Hmv05401.app
Output Set: N:\CRF4\06232003\I908992A.raw

```
129 atc ccc cct ggg act cag aca gac cag aag att cgg atg ggt ggg aaa  1204
130 Ile Pro Pro Gly Thr Gln Thr Asp Gln Lys Ile Arg Met Gly Gly Lys
131               380              385                  390
133 ggc atc ccc cgg att aac agc tac ggc tac gga gac cac tac atc cac  1252
134 Gly Ile Pro Arg Ile Asn Ser Tyr Gly Tyr Gly Asp His Tyr Ile His
135               395              400                  405
137 atc aag ata cga gtt cca aag agg cta acg agc cgg cag cag agc ctg  1300
138 Ile Lys Ile Arg Val Pro Lys Arg Leu Thr Ser Arg Gln Gln Ser Leu
139           410              415                  420
141 atc ctg agc tac gcc gag gac gag aca gat gtg gag ggg acg gtg aac  1348
142 Ile Leu Ser Tyr Ala Glu Asp Glu Thr Asp Val Glu Gly Thr Val Asn
143       425              430                  435
145 ggc gtc acc ctc acc agc tct ggt ggc agc acc atg gat agc tcc gca  1396
146 Gly Val Thr Leu Thr Ser Ser Gly Gly Ser Thr Met Asp Ser Ser Ala
147 440               445              450                  455
149 gga agc aag gct agg cgt gag gct ggg gag gac gag gag gga ttc ctt  1444
150 Gly Ser Lys Ala Arg Arg Glu Ala Gly Glu Asp Glu Glu Gly Phe Leu
151               460              465                  470    .
153 tcc aaa ctt aag aaa atg ttt acc tca tgatatccca gccgaggaaa       1491
154 Ser Lys Leu Lys Lys Met Phe Thr Ser
155               475              480
157 aagatccact ggaaactagg ccgggaagca gcagcccctc caagggccag ggcacctggg 1551
159 agacgggagg attccagaac agcagcactg agctcccacc cgcagagcct ctggacggcc 1611
161 ttggcaacag caaaatcatg ggacaacacc tctctccacg gaaaggtcac agtggacagc 1671
163 ccgggcagta ggatgcagcc ccagaggctg gtggcagttt cctgtccatt ggtaggtgac 1731
165 ggccccctgg tcagcagagg agaggttaga tcttgcaggc taaaactcta atttggaatt 1791
167 gaatattgtg gatatcttag ttaaaggcca tgcttacagc ttagaaatga agccttaagc 1851
169 tgcatcaagt tacgaagtga ttaatttcct tctcagcaaa cctccgggag gttccagaat 1911
171 gagttcttcc tgacaggttg tcttcactgg gagcgtgggg cccccaggcc ccaccagcac 1971
173 cgtcctcccc taatgagggg ccctgccgag gcatcagctg ctctgctcag ttagttttta 2031
175 ttcccggggt accaagcagc tgcacagtcg gtgcctggga agcacgttaa aggcccagag 2091
177 agatcctggg ggttctgctc tgaccgtgtg ggtggtgatc cttgtcagga tgtacagtcc 2151
179 ttgctcccac cccatccggg atggccgcct gtccctgact attgagtcct gttgttgtaa 2211
181 gccaggcatg gagggctcct gcccttctgc tgagccacag cccattgcag cactgtgctg 2271
183 gccagacttc agctgccttg ggaactgaag ccctgccact gttgctagtc aggggcttgg 2331
185 ttctcccact tacactgttg acatctattt tctgaagtgt gtttaaatta ttcagtgcta 2391
187 atcattgttt tttcctttgt aaatgttgat tcagaaaagg aaagcacagg ctaagcagtt 2451
189 gaaggttccc caccattcag tgagagcaga accccccattc cccagcctct gctggtagca 2511
191 tgtcgcagtt tccatgtgtt tcaggatctt cgggctgtcg ttagacaggt taatgaagaa 2571
193 cacttctcaa cagtttcctt tttgttttcc tttataattc actaaaataa agcatctatt 2631
195 agtgtctgaa aaaaaaaaaa aaaaa                                        2656
198 <210> SEQ ID NO: 2
199 <211> LENGTH: 1443
200 <212> TYPE: DNA
201 <213> ORGANISM: Homo sapiens
203 <220> FEATURE:
204 <221> NAME/KEY: CDS
205 <222> LOCATION: (1)..(1440)
207 <400> SEQUENCE: 2
```

```
208 atg gct gcg cgg tgc tcc aca cgc tgg ttg ctg gtg gtt gtg ggg acc   48
209 Met Ala Ala Arg Cys Ser Thr Arg Trp Leu Leu Val Val Val Gly Thr
210  1               5                  10                  15
212 ccg cgg ctg ccg gct ata tcg ggt aga ggg gcc cgg ccg ccc agg gag   96
213 Pro Arg Leu Pro Ala Ile Ser Gly Arg Gly Ala Arg Pro Pro Arg Glu
214              20                  25                  30
216 ggc gtg gtg ggg gca tgg ctg agc cgc aag ctg agc gtc ccc gcc ttt  144
217 Gly Val Val Gly Ala Trp Leu Ser Arg Lys Leu Ser Val Pro Ala Phe
218          35                  40                  45
220 gcg tct tcc ctg acc tct tgc ggc ccc cga gcg ctg ctg aca ttg aga  192
221 Ala Ser Ser Leu Thr Ser Cys Gly Pro Arg Ala Leu Leu Thr Leu Arg
222      50                  55                  60
224 cct ggt gtc agc ctt aca gga aca aaa cat aac cct ttc att tgt act  240
225 Pro Gly Val Ser Leu Thr Gly Thr Lys His Asn Pro Phe Ile Cys Thr
226  65                  70                  75                  80
228 gcc tcc ttc cac acg agt gcc cct ttg gcc aaa gaa gat tat tat cag  288
229 Ala Ser Phe His Thr Ser Ala Pro Leu Ala Lys Glu Asp Tyr Tyr Gln
230              85                  90                  95
232 ata tta gga gtg cct cga aat gcc agc cag aaa gag atc aag aaa gcc  336
233 Ile Leu Gly Val Pro Arg Asn Ala Ser Gln Lys Glu Ile Lys Lys Ala
234          100                 105                 110
236 tat tat cag ctt gcc aag aag tat cac cct gac aca aat aag gat gat  384
237 Tyr Tyr Gln Leu Ala Lys Lys Tyr His Pro Asp Thr Asn Lys Asp Asp
238          115                 120                 125
240 ccc aaa gcc aag gag aag ttc tcc cag ctg gca gaa gcc tat gag gtt  432
241 Pro Lys Ala Lys Glu Lys Phe Ser Gln Leu Ala Glu Ala Tyr Glu Val
242      130                 135                 140
244 ttg agt gat gag gtg aag agg aag cag tac gat gcc tac ggc tct gca  480
245 Leu Ser Asp Glu Val Lys Arg Lys Gln Tyr Asp Ala Tyr Gly Ser Ala
246 145                 150                 155                 160
248 ggc ttc gat cct ggg gcc agc ggc tcc cag cat agc tac tgg aag gga  528
249 Gly Phe Asp Pro Gly Ala Ser Gly Ser Gln His Ser Tyr Trp Lys Gly
250              165                 170                 175
252 ggc ccc act gtg gac ccc gag gag ctg ttc agg aag atc ttt ggc gag  576
253 Gly Pro Thr Val Asp Pro Glu Glu Leu Phe Arg Lys Ile Phe Gly Glu
254              180                 185                 190
256 ttc tca tcc tct tca ttt gga gat ttc cag acc gtg ttt gat cag cct  624
257 Phe Ser Ser Ser Ser Phe Gly Asp Phe Gln Thr Val Phe Asp Gln Pro
258          195                 200                 205
260 cag gaa tac ttc atg gag ttg aca ttc aat caa gct gca aag ggg gtc  672
261 Gln Glu Tyr Phe Met Glu Leu Thr Phe Asn Gln Ala Ala Lys Gly Val
262      210                 215                 220
264 aac aag gag ttc acc gtg aac atc atg gac acg tgt gag cgc tgc aac  720
265 Asn Lys Glu Phe Thr Val Asn Ile Met Asp Thr Cys Glu Arg Cys Asn
266 225                 230                 235                 240
268 ggc aag ggg aac gag ccc ggc acc aag gtg cag cat tgc cac tac tgt  768
269 Gly Lys Gly Asn Glu Pro Gly Thr Lys Val Gln His Cys His Tyr Cys
270              245                 250                 255
272 ggc ggc tcc ggc atg gaa acc atc aac aca ggc cct ttt gtg atg cgt  816
```

Input Set : A:\Hmv05401.app
Output Set: N:\CRF4\06232003\I908992A.raw

```
273 Gly Gly Ser Gly Met Glu Thr Ile Asn Thr Gly Pro Phe Val Met Arg
274             260             265             270
276 tcc acg tgt agg aga tgt ggt ggc cgc ggc tcc atc atc ata tcg ccc    864
277 Ser Thr Cys Arg Arg Cys Gly Gly Arg Gly Ser Ile Ile Ile Ser Pro
278             275             280             285
280 tgt gtg gtc tgc agg gga gca gga caa gcc aag cag aaa aag cga gtg    912
281 Cys Val Val Cys Arg Gly Ala Gly Gln Ala Lys Gln Lys Lys Arg Val
282     290             295             300
284 atg atc cct gtg cct gca gga gtc gag gat ggc cag acc gtg agg atg    960
285 Met Ile Pro Val Pro Ala Gly Val Glu Asp Gly Gln Thr Val Arg Met
286 305             310             315             320
288 cct gtg gga aaa agg gaa att ttc att acg ttc agg gtg cag aaa agc   1008
289 Pro Val Gly Lys Arg Glu Ile Phe Ile Thr Phe Arg Val Gln Lys Ser
290             325             330             335
292 cct gtg ttc cgg agg gac ggc gca gac atc cac tcc gac ctc ttt att   1056
293 Pro Val Phe Arg Arg Asp Gly Ala Asp Ile His Ser Asp Leu Phe Ile
294             340             345             350
296 tct ata gct cag gct ctt ctt ggg gga aca gcc aga gcc cag ggc ctg   1104
297 Ser Ile Ala Gln Ala Leu Leu Gly Gly Thr Ala Arg Ala Gln Gly Leu
298             355             360             365
300 tac gag acg atc aac gtg acg atc ccc cct ggg act cag aca gac cag   1152
301 Tyr Glu Thr Ile Asn Val Thr Ile Pro Pro Gly Thr Gln Thr Asp Gln
302     370             375             380
304 aag att cgg atg ggt ggg aaa ggc atc ccc cgg att aac agc tac ggc   1200
305 Lys Ile Arg Met Gly Gly Lys Gly Ile Pro Arg Ile Asn Ser Tyr Gly
306 385             390             395             400
308 tac gga gac cac tac atc cac atc aag ata cga gtt cca aag agg cta   1248
309 Tyr Gly Asp His Tyr Ile His Ile Lys Ile Arg Val Pro Lys Arg Leu
310             405             410             415
312 acg agc cgg cag cag agc ctg atc ctg agc tac gcc gag gac gag aca   1296
313 Thr Ser Arg Gln Gln Ser Leu Ile Leu Ser Tyr Ala Glu Asp Glu Thr
314             420             425             430
316 gat gtg gag ggg acg gtg aac ggc gtc acc ctc acc agc tct ggt ggc   1344
317 Asp Val Glu Gly Thr Val Asn Gly Val Thr Leu Thr Ser Ser Gly Gly
318             435             440             445
320 agc acc atg gat agc tcc gca gga agc aag gct agg cgt gag gct ggg   1392
321 Ser Thr Met Asp Ser Ser Ala Gly Ser Lys Ala Arg Arg Glu Ala Gly
322     450             455             460
324 gag gac gag gag gga ttc ctt tcc aaa ctt aag aaa atg ttt acc tca   1440
325 Glu Asp Glu Glu Gly Phe Leu Ser Lys Leu Lys Lys Met Phe Thr Ser
326 465             470             475             480
328 tga                                                               1443
331 <210> SEQ ID NO: 3
332 <211> LENGTH: 1362
333 <212> TYPE: DNA
334 <213> ORGANISM: Homo sapiens
336 <220> FEATURE:
337 <221> NAME/KEY: CDS
338 <222> LOCATION: (1)..(1359)
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 06/23/2003
PATENT APPLICATION: US/09/908,992A   TIME: 14:58:15

Input Set : **A:\Hmv05401.app**
Output Set: **N:\CRF4\06232003\I908992A.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:28; Xaa Pos. 206,207,208,209,210,211,212,213,214,215,216,217,218,219
Seq#:28; Xaa Pos. 220,221,222,223,224
Seq#:29; Xaa Pos. 206,207,208,209,210,211,212,213,214,215,216,217,218,219
Seq#:29; Xaa Pos. 220,221,222,223,224